REMARKS

The May 30, 2001 Official Action and references cited therein have been carefully reviewed. In view of the amendments submitted herewith and the following remarks, favorable reconsideration and allowance of this application are respectfully requested.

Status of the claims and prosecution:

Claims 1-11, 13-17, 25 and 26 are currently pending. In the May 30, 2001 Official Action, all pending claims were finally rejected, and certain objections to the specification were made.

Applicants' amendment filed March 5, 2001 was objected to under 35 U.S.C. §132 for allegedly introducing new matter into the specification. Specifically, the examiner asserts that the phrase "non-mammalian" in amended claims 7 and 14 and the recitation of specific nucleotide positions in amended claim 11 are not supported by the specification.

For the reasons cited in the objection to the 3/5/01 amendment, claims 7 and 11-17 also stand rejected under 35 U.S.C. §112, first paragraph, for alleged lack of adequate written description.

Claims 1-11, 13-17, 25 and 26 remain rejected under 35 U.S.C. §112, first paragraph, for alleged lack of adequate written description, for the reasons set forth in the first Official Action of September 7, 2000. Applicants' amendments and arguments submitted March 5, 2001 were not found persuasive to overcome the rejection.

Claims 1-11, 13-17, 25 and 26 remain rejected under 35 U.S.C. §112, first paragraph, for alleged lack of enablement, for the reasons set forth in the first Official Action of September 7, 2000. Applicants' amendments and arguments submitted March 5, 2001 were not found persuasive to overcome the rejection.

Claims 2, 6-10, 13-17 and 25 are newly rejected or remain rejected under 35 U.S.C. §112, second paragraph, for alleged indefiniteness on various grounds. Specifically, claim 2 is allegedly indefinite in the recitation of "60% identical to SEQ ID NO:1" followed by the recitation of hybridization conditions. Claims 6 and 13 are deemed indefinite in the recitation of "operably linked to a vector". Claim 11 is deemed indefinite in its recitation of "high stringency". Claim 25 is allegedly indefinite in its recitation of "*AVR1-CO39*" in referring to the claimed gene.

Claims 11 and 13-16 remain rejected under 35 U.S.C. §102(b) as allegedly anticipated by Shimizu et al., Infect. Immunol. 59: 137-142, 1991. Applicants' arguments filed March 5, 2001 were found unpersuasive to overcome the rejection.

The present Amendment and Request for Reconsideration accompanies a Request for Continued Examination (RCE). The claims have been amended as follows.

Claim 1 has been amended to specify that the isolated nucleic acid molecule claimed therein hybridizes with SEQ ID NO:1 or its complement under hybridization conditions comprising hybridization at 42°C in 5X SSC, 5X Denhardt's reagent, 1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and 50% formamide and washing

at 55°C in 2X SSC and 0.1% SDS. Support for the hybridization conditions now recited in claim 1 is found in the specification at page 14, lines 1-13.

Claim 2 has been amended to further delimit specific regions of SEQ ID NO:1 or its complement, to which the claimed nucleic acid molecule hybridizes, and to include a more stringent washing step in the hybridization conditions. Support for the more stringent washing step is found in the specification at page 23, lines 27-28. Support for the recited specific regions of SEQ ID NO:1 or its complement is found at page 27, lines 1-44. Page 27 displays SEQ ID NO:1 and indicates the starting position, reading direction, and termination position of each of the seven open reading frames delimited in claim 2. The positions of these start and termination positions are referenced to the first nucleotide of SEQ ID NO:1, as is customary in the art.

Claim 3 has been amended to further specify that the isolated nucleic acid molecule of claim 2 comprises one or more of the specific regions recited in claim 2.

Claim 4 has not been further amended. Claim 5 was redundant of claim 4 as previously amended. Hence, claim 5 has now been amended to recite that the isolated nucleic acid molecule encodes SEQ ID NO:4.

Claims 6 and 13 have been amended to replace the term "operably linked to" with the term "inserted into". Support for this amendment is found in the specification at page 6, lines 15-17 and at page 16, lines 8-19.

Claims 7 and 14 have been amended to replace the term "non-mammalian" with the recitation "fungal, bacterial, or plant". Claims 8-9 and 15-16 have been amended for proper dependence from claims 7 and 14, respectively.

Claim 11 has been amended to recite the specific hybridization and washing conditions constituting "high stringency". Support for this claim amendment is found in the specification at page 23, lines 16-33.

Claim 25 has been amended to replace the recitation of "an *AVR1-CO39* gene" with the description of the gene as now set forth in claim 1. Claim 26 has been amended to add that the gene of claim 25 encodes SEQ ID NO:2 or SEQ ID NO:4. Support for the amendment to claim 26 is found in the specification at page 29, lines 14-23.

Applicants assert that the amendments to claims 1-11, 13-17, 25 and 26 overcome each of the objections and rejections issued in the May 30, 2001 official action, and that the claims as amended are in condition for allowance. Support for Applicants' assertion to this effect is set forth below.

Objection to the specification and related rejection under 35 U.S.C. §112, first paragraph:

As a result of the claim amendments submitted March 5, 2001, the specification was objected to under 35 U.S.C. §132 and claims 7 and 11-17 were rejected under 35 U.S.C. §112, first paragraph, for addition of allegedly new matter in the recitation of "non-mammalian" and for the recitation of specific nucleotide positions.

Claims 7 and 14 have been amended such that the term "non-mammalian" no longer appears. Accordingly, the objection and rejection on this ground should be overcome, and Applicants request its withdrawal.

Applicants traverse the objection and rejection on the ground that recitation of specific nucleotide positions in the claims constitutes new matter. This information is not new matter inasmuch as support for the specific nucleotide positions currently recited in the claims is obtained from the originally-filed specification at page 27, lines 1-44. Page 27 displays SEQ ID NO:1 and indicates the starting position, reading direction, and termination position of each of the seven open reading frames delimited in the claims. The positions of these start and termination positions are referenced to the first nucleotide of SEQ ID NO:1, as is customary in the art. Thus, even though the specification does not recite this information word-for-word, i.e., "position X - X" of SEQ ID NO:1, the information is implicit in, and easily obtainable from, the annotated sequence of SEQ ID NO:1 set forth at page 27. The disclosure at page 27 of the specification is clearly sufficient to convey to a person of ordinary skill in the art that the applicants invented the subject matter of claim 11 (and newly-amended claims 2 and 3). Nothing more is required under 35 U.S.C. §112, first paragraph. Accordingly, withdrawal of the objection and rejection on this ground is requested.

Rejection under 35 U.S.C. §112, first paragraph (written description):

Claims 1-11, 13-17, 25 and 26 remain rejected under 35 U.S.C. §112, first paragraph, for alleged lack of adequate written description. In particular, the examiner continues to assert that it

is not clear from the specification that the applicants were in possession of the invention as claimed. Further, the examiner asserts that the present specification does not describe a representative number of the claimed genus or structural motifs common to members of the genus, so as to allow one of skill in the art to recognize other nucleic acid sequences of the claimed genus.

Applicants traverse this rejection as applied to the claims as presently amended. Claim 1 recites an isolated nucleic acid molecule with specific structural and functional features. Functionally, it is a *M. grisea* nucleic acid molecule that confers rice cultivar CO39-specific avirulence to fungal plant pathogens. Structurally, it is a 1-Kb segment, it contains at least one open reading frame, and it comprises a sequence that hybridizes under specified conditions to SEQ ID NO:1. Claim 25 recites an epiphytic bacterium comprising the nucleic acid molecule described in claim 1. Claim 11 recites a group of nucleic acid molecules whose sequence features are either specifically recited, or recited in terms of their ability to hybridize with specific sequences under specific high-stringency conditions. These functional and structural features are set forth throughout the specification. Further, though the specification describes the sequence of only one member of the claimed genus, it nevertheless describes more than one member of the genus. As set forth in Example 3, homologs of SEQ ID NO:1 were found in *M. grisea* isolates that infect Setaria. These homologs were identified using hybridization conditions as set forth in Example 1 of the application, and as specified in claim 2 and claim 11, as presently amended.

For the foregoing reasons, Applicants submit that the presently amended claims are described in the specification in such a way as to convey to one of skill in the art that the Applicants were in

possession of the claimed invention at the time the application was filed. Therefore, the written description requirement of 35 U.S.C. §112, first paragraph, is satisfied and Applicants request withdrawal of the rejection on this ground.

Rejection under 35 U.S.C. §112, first paragraph (enablement):

Claims 1-11, 13-17, 25 and 26 remain rejected under 35 U.S.C. §112, first paragraph, for alleged lack of enablement. In particular, the examiner asserts that the specification is enabling only for claims limited to an isolated nucleic acid molecule encoding SEQ ID NO:4 and transformed cells and transgenic plants comprising the nucleic acid molecule.

Applicants traverse this rejection as it applies to the claims as presently amended. The amended claims call for either specific nucleotide sequences (or sequences encoding specific amino acid sequences, or nucleic acid molecules that hybridize with the disclosed sequences under particular hybridization conditions. SEQ ID NO:1 is taught in the specification at page 27 and elsewhere. The open reading frames of SEQ ID NO:1 are taught at page 27. Hybridization conditions for isolating nucleic acid molecules that are within the scope of the presently amended claims are taught at pages 14 and 23 of the specification. The ability of SEQ ID NO:1 to confer CO39 cultivar specificity to an organism is taught in Example 1. The specific role of ORF1 (SEQ ID NO:2) and ORF3 (SEQ ID NO:4) in conferring cultivar-specific avirulence is taught in Example 1. A method of determining if such cultivar specificity is conferred by an isolated nucleic acid molecule is also taught in Example 1. With this combination of teachings, one of skill in the art

would be able to identify and obtain isolated nucleic acid molecules that (1) have at least one ORF, (2) confer CO39 cultivar specific avirulence, and (3) hybridize under the recited specific hybridization conditions recited in the claims, without undue experimentation. The examiner has asserted that this is not the case because Applicants engaged in significant experimentation to identify SEQ ID NO:1 in the first place. This is true, and it is the reason why the present invention discloses novel and inventive subject matter. However, it is not relevant to whether the specification is enabling for the invention as claimed. That standard has been met by the above-listed teachings of the specification. Once SEQ ID NO:1 was obtained and characterized in accordance with the present invention, the ability to obtain similar nucleic acid molecules within the scope of the claims became possible. The specification teaches how to do this, such that the invention in its present scope may be practiced without undue experimentation, thereby meeting the enablement requirement of 35 U.S.C. §112, first paragraph. Accordingly, withdrawal of the rejection on this ground is requested.

The examiner also asserts that the specification enables only claims to fungal, bacterial or plant cells transformed with the claimed nucleic acid molecule. The claims have been amended to recite fungal, bacterial and plant cells transformed with the claimed nucleic acid molecule. Therefore, the rejection on this ground should be overcome, and its withdrawal is requested.

Rejection under 35 U.S.C. §112, second paragraph:

Claims 2, 6-10, 13-17 and 25 stand rejected under 35 U.S.C. §112, second paragraph, for alleged indefiniteness.

Claim 2 was deemed indefinite in its recitation of "60% identical to SEQ ID NO:1" followed by a recitation of hybridization conditions. Claim 2 has been amended so that it no longer calls for a nucleic acid molecule with 60% identity to SEQ ID NO:1. Therefore, this ground of rejection should be overcome, and its withdrawal is requested.

Claims 6 and 13 were deemed indefinite in their recitation of "operably linked to" a vector. That terminology has been replaced by the phrase "inserted into." Therefore, this ground of rejection should be overcome, and its withdrawal is requested.

Claim 11 was deemed indefinite in its recitation of "high stringency" on the examiner's assertion that "high" is a relative term. Claim 11 has been amended to recite hybridization and washing conditions. Applicants assert that the metes and bounds of the invention claimed in claim 11 are clear. Accordingly, withdrawal of the rejection on this ground is requested.

Claim 25 was deemed indefinite in its reference to the claimed gene by the name "*AVR1-CO39*". Claim 25 has been amended so that the nucleic acid molecule recited therein is not described by the name, but instead is described as in claim 1. Applicants assert that the metes and bounds of the invention claimed in claim 25 are clear. Accordingly, withdrawal of the rejection on this ground is requested.

Rejection under 35 U.S.C. §102(b):

Claims 11 and 13-16 remain rejected under 35 U.S.C. §102(b) as allegedly anticipated by Shimizu et al. (1991). In Applicants' previous response, Applicants amended claim 11 to remove the term "part or all", and asserted that the claim amendment rendered claims 11 and 13-16 not anticipated by Shimizu et al. In the May 30, 2001 Action, the examiner responds that, in view of the alleged indefiniteness of the claim limitation "high stringency", the claims still read on the prior art reference.

Claim 11 has now been amended to specify the hybridization conditions referred to as "high stringency" in the previous amendment. As set forth at page 23, lines 16-33, the hybridization conditions now specified in claim 11 are sufficiently stringent that a hybrid of less than 95% homology would not be maintained. The examiner still has not pointed to the sequence or sequences disclosed by Shimizu et al. that form the basis of this rejection. However, Applicants assert that none of the sequences of Shimizu et al. is identical to the sequences recited in claim 11, in view of the hybridization conditions now set forth in the claims. Accordingly, the rejection of claims 11 and 13-16 under 35 U.S.C. §102(b) based on Shimizu et al. should be withdrawn.

In view of the claim amendments submitted herewith and the foregoing remarks, the presently-pending claims are believed to be in condition for allowance. Applicants respectfully request early and favorable reconsideration and withdrawal of the objections and rejections set forth in the May 30, 2001 Official Action, and allowance of this application.

DOCKET NO.: WARF-0071/(P98067US) **PATENT**

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned **"Version with markings to show changes made."**

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

1. (Twice amended) An isolated nucleic acid molecule from *Magnaporthe grisea* comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the segment conferring rice cultivar CO39-specific avirulence to fungal plant pathogens that contain the nucleic acid, wherein the nucleic acid molecule hybridizes with SEQ ID NO:1 or its complement under hybridization conditions comprising hybridization at 42°C in 5X SSC, 5X Denhardt's reagent, 1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and 50% formamide and washing at 55°C in 2X SSC and 0.1% SDS.

2. (Twice amended) The nucleic acid molecule of claim 1, having a nucleotide sequence that hybridizes with a portion of SEQ ID NO:1 or its complement, wherein the portion is selected from the group consisting of :

an open reading frame located between nucleotide 358 and 495;

an open reading frame located between nucleotide 443 and 676;

an open reading frame located between nucleotides 582 and 850;

an open reading frame located between nucleotides 753 and 858;

an open reading frame located between nucleotides 885 and 1047;

an open reading frame on the complementary strand of SEQ ID NO:1 located between nucleotides 757 and 561;

an open reading frame on the complementary strand of SEQ ID NO: 1 located between nucleotides 419 and 312;

wherein the hybridization conditions further comprise washing in 0.1X SSC, 0.1% SDS at 65°C

[at least 60% identical to SEQ ID NO:1, the identity being calculated by hybridization with SEQ ID NO:1 under conditions derived from a formula of:

$T_m = 81.5°C + 16.6 \text{ Log} + 0.41 (\%G+C) - 0.63 (\% \text{ formamide}) - 600 / \#bp \text{ in duplex.}]$

3. (Amended) The nucleic acid molecule of claim 2, comprising a portion of SEQ ID NO:1, wherein the portion is selected from the group consisting of :

an open reading frame located between nucleotide 358 and 495;

an open reading frame located between nucleotide 443 and 676;

an open reading frame located between nucleotides 582 and 850;

an open reading frame located between nucleotides 753 and 858;

an open reading frame located between nucleotides 885 and 1047;

an open reading frame on the complementary strand of SEQ ID NO:1 located between nucleotides 757 and 561;

an open reading frame on the complementary strand of SEQ ID NO: 1 located between nucleotides 419 and 312 [having a sequence comprising part or all of SEQ ID NO:1].

5. (Amended) The nucleic acid molecule of claim 4, which encodes a polypeptide having [a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3,] SEQ ID NO:4[, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8].

6. (Amended) A recombinant DNA molecule comprising the nucleic acid molecule of claim 1, inserted into [operably linked to] a vector for transforming cells.

7. (Twice amended) A fungal, bacterial, or plant [non-mammalian] cell transformed with the recombinant DNA molecule of claim 6.

8. (Twice amended) The cell of claim 7, which is a plant cell that is regenerable into a fertile plant [wherein said cell is either bacterial, fungal, insect or plant].

9. (Twice amended) The cell of claim 7 [8], which is an epiphytic bacterial cell.

11. (Twice amended) An isolated nucleic acid molecule having a sequence selected from the group consisting of:

a) SEQ ID NO:1;

b) an allelic variant of an isolated nucleic acid comprising SEQ ID NO:1;

c) a segment of SEQ ID NO: 1 selected from the group consisting of:

an open reading frame located between nucleotide 358 and 495;

an open reading frame located between nucleotide 443 and 676;

an open reading frame located between nucleotides 582 and 850;

an open reading frame located between nucleotides 753 and 858;

an open reading frame located between nucleotides 885 and 1047;

an open reading frame on the complementary strand of SEQ ID NO:1 located between nucleotides 757 and 561;

an open reading frame on the complementary strand of SEQ ID NO: 1 located between nucleotides 419 and 312;

d) an allelic variant of the segment of SEQ ID NO:1;

e) a sequence that hybridizes with any of the sequences of a) - d) or its complement under [high stringency] conditions comprising hybridization at 42°C in 5X SSC, 5X Denhardt's reagent, 7% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.125M NaHPO4, 50% formamide and 1 mM EDTA, rinsing with 2X SSC at room temperature, and washing at 65°C in 2X SSC, followed by 65°C in 0.1X SSC and 0.1% SDS.; and

f) a sequence encoding a polypeptide having an amino acid sequence comprising any one of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

13. (Amended) A recombinant DNA molecule comprising the nucleic acid molecule of claim 11, inserted into [operably linked to] a vector for transforming cells.

14. (Twice amended) A bacterial, fungal, or plant [non-mammalian] cell transformed with the recombinant DNA molecule of claim 13.

15. (Twice amended) The cell of claim 14, which is a plant cell that is regenerable into a fertile plant [wherein said cell is either bacterial, insect, yeast or plant].

16. (Amended) The cell of claim 14 [15], which is an epiphytic bacterial cell.

25. (Amended) A transgenic epiphytic bacterium that expresses a portion of an isolated nucleic acid molecule from *Magnaporthe grisea* comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the segment conferring rice cultivar CO39-specific avirulence to microorganisms that contain the nucleic acid, wherein the nucleic acid molecule hybridizes with SEQ ID NO:1 under hybridization

conditions comprising hybridization at 42°C in 5X SSC, 5X Denhardt's reagent, 1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and 50% formamide and washing at 55°C in 2X SSC and 0.1% SDS. [an *AVR1-CO39* gene which confers rice cultivar CO39-specific avirulence to microorganisms expressing the gene].

26. (Twice amended) The transgenic epiphytic bacterium of claim 24, which expresses the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, or an allelic variant thereof.